TEAM 8

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/779,599*

DATE: 03/04/97
TIME: 13:58:01

INPUT SET: S15900.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

```
 1                           SEQUENCE LISTING
 2
 3   (1)    General Information:
 4
 5     (i) APPLICANT: Goeddel, David V.
 6                   Rothe. Mike
 7
 8    (ii) TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
 9                  -
10   (iii) NUMBER OF SEQUENCES: 59
11
12    (iv) CORRESPONDENCE ADDRESS:
13         (A) ADDRESSEE: Genentech, Inc.
14         (B) STREET: 460 Point San Bruno Blvd
15         (C) CITY: South San Francisco
16         (D) STATE: California
17         (E) COUNTRY: USA
18         (F) ZIP: 94080
19
20     (v) COMPUTER READABLE FORM:
21         (A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
22         (B) COMPUTER: IBM PC compatible
23         (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24         (D) SOFTWARE: WinPatin (Genentech)
25
26    (vi) CURRENT APPLICATION DATA:
27         (A) APPLICATION NUMBER:
28         (B) FILING DATE: 07-Jan-1997
29         (C) CLASSIFICATION:
30
31  (viii) ATTORNEY/AGENT INFORMATION:
32         (A) NAME: Dreger, Ginger R.
33         (B) REGISTRATION NUMBER: 33,055
34         (C) REFERENCE/DOCKET NUMBER: P0897C2
35
36    (ix) TELECOMMUNICATION INFORMATION:
37         (A) TELEPHONE: 415/225-3216
38         (B) TELEFAX: 415/952-9881
39         (C) TELEX: 910/371-7168
40
41  (2) INFORMATION FOR SEQ ID NO:1:
42
43     (i) SEQUENCE CHARACTERISTICS:
44         (A) LENGTH: 2088 base pairs
45         (B) TYPE: Nucleic Acid
46         (C) STRANDEDNESS: Single
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RAW SEQUENCE LISTING
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47          (D) TOPOLOGY: Linear
48
49      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
50
51
52    CCCAGCCCGG TTCTCTGCCC CAAGGACGCT ACCGCCCAAT GCGAGCAGAA  50
53
54    GGCGGCGCAC AGATACAGAA AGTGAGGCTC AGACATATTG AAGACCGTGT  100
55
56    GACATAGGGT AGCCAAATGA CAGTGTGAGA AAGTGACATT TACTCAAGGC  150
57
58    CACCCAGATA TCCTGGAGGA CCCAGAACCC TGGAGATTCC CATCAGAAAG  200
59
60    ACCTTCTGGC CACCTGAAAC CCCAAGATGG CCTCCAGCTC AGCCCCTGAT  250
61
62    GAAAACGAGT TTCAATTTGG TTGCCCCCCT GCTCCCTGCC AGGACCCATC  300
63
64    GGAGCCCAGA GTTCTCTGCT GCACAGCCTG TCTCTCTGAG AACCTGAGAG  350
65
66    ATGATGAGGA TCGGATCTGT CCTAAATGCA GAGCAGACAA CCTCCATCCT  400
67
68    GTGAGCCCAG GAAGCCCTCT GACTCAGGAG AAGGTTCACT CTGATGTAGC  450
69
70    TGAGGCTGAA ATCATGTGCC CCTTTGCAGG TGTTGGCTGT TCCTTCAAGG  500
71
72    GGAGCCCACA ATCCATGCAG GAGCATGAGG CTACCTCCCA GTCCTCCCAC  550
73
74    CTGTACCTGC TGCTGGCGGT CTTAAAGGAG TGGAAATCCT CACCAGGCTC  600
75
76    CAACCTAGGG TCTGCACCCA TGGCACTGGA GCGGAACCTG TCAGAGCTGC  650
77
78    AGCTTCAGGC AGCTGTGGAA GCGACAGGGG ACCTGGAGGT AGACTGCTAC  700
79
80    CGGGCACCTT GCTGTGAGAG CCAGGAAGAA CTGGCCCTGC AGCACTTGGT  750
81
82    GAAGGAGAAG CTGCTGGCTC AGCTGGAGGA GAAGCTGCGT GTGTTTGCAA  800
83
84    ACATTGTTGC TGTCCTCAAC AAGGAAGTGG AGGCTTCCCA CCTGGCACTG  850
85
86    GCCGCCTCCA TCCACCAGAG CCAGTTGGAC CGAGAGCACC TCCTGAGCTT  900
87
88    GGAGCAGAGG GTGGTGGAAT TACAGCAAAC CCTGGCTCAA AAAGACCAGG  950
89
90    TCCTGGGCAA GCTTGAGCAC AGTCTGCGAC TCATGGAGGA GGCATCCTTT  1000
91
92    GATGGTACTT TCCTGTGGAA GATCACCAAT GTCACCAAGC GGTGCCACGA  1050
93
94    GTCAGTGTGT GGCCGGACTG TCAGCCTCTT CTCTCCAGCT TTCTACACTG  1100
95
96    CCAAGTATGG TTACAAGTTG TGCCTGCGCT TGTACCTGAA CGGGGATGGC  1150
97
98    TCAGGCAAGA AGACCCACCT GTCCCTCTTC ATCGTGATCA TGAGAGGAGA  1200
99
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INPUT SET: S15900.raw

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100     ATACGATGCT CTCCTGCCCT GGCCTTTCAG GAACAAGGTC ACCTTTATGC 1250
101
102     TACTTGACCA GAACAACCGA GAGCATGCTA TTGATGCCTT CCGGCCTGAC 1300
103
104     CTGAGCTCAG CCTCCTTCCA GCGGCCACAG AGTGAGACCA ACGTGGCCAG 1350
105
106     CGGCTGCCCG CTCTTCTTCC CCCTCAGCAA GCTGCAGTCA CCCAAGCACG 1400
107
108     CCTACGTCAA AGATGACACA ATGTTCCTCA AATGCATTGT GGACACTAGT 1450
109
110     GCTTAGGGAT GGGGGGAGGG GGTGTCTCCT GACAGAACCA GCTTAGACTG 1500
111
112     GGGGACTTAG CTAGACAGCC AGGCCCTGCC TGCCCTTGGA GCCCACAGCC 1550
113
114     CACGACAAGG AGGAGCCAAG GCTGGCATGA CTTCAGCGCC ACAGCATGCT 1600
115
116     GGTTATGGCT GATGTGAGGC TGGAGAAACG TGTGCGTACA GAGACAGAGT 1650
117
118     GGAGGAGAAG ACAGAAGTGC TCTTTTCACA CAGACTACAC GACACCAGGA 1700
119
120     GGCCAGCATG CCAGCAGCTT CTGAATGTTG AGACCAGCCT AGATCAGGAT 1750
121
122     GAAAAGAGCC AGGCCTGAGG CTTGGACATT GAGCCAAGGC TATGGGGCCT 1800
123
124     AAGTGGAGGG GCACTCCTAC CAGGACATTC TCTCGAGGTC AGGGCATAAC 1850
125
126     TGGAAAAATG CCCCCATCTC TCTGTTCAGA CTCAAAACTA GAACCACAGG 1900
127
128     GCAGAAGGGT CAGACATTAA TGTGAATTTA ACCTGCCCTG GACTGAGTTC 1950
129
130     CTATGTTAAC AGACACGCAA ACAGGTAAAC CCAGAAACTG CCCTGGGAAA 2000
131
132     TGCTTTCTGG CTGCATCTGG AGATCTTTGA TGTTTTTACC GACAAAACAA 2050
133
134     ATAACAAAAG CCTTGAATTG CAAAAAAAAA AAAAAAA 2088
135
136     (2) INFORMATION FOR SEQ ID NO:2:
137
138         (i) SEQUENCE CHARACTERISTICS:
139             (A) LENGTH: 409 amino acids
140             (B) TYPE: Amino Acid
141             (D) TOPOLOGY: Linear
142
143         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
144
145     Met Ala Ser Ser Ser Ala Pro Asp Glu Asn Glu Phe Gln Phe Gly
146      1               5                   10                  15
147
148     Cys Pro Pro Ala Pro Cys Gln Asp Pro Ser Glu Pro Arg Val Leu
149                     20                  25                  30
150
151     Cys Cys Thr Ala Cys Leu Ser Glu Asn Leu Arg Asp Asp Glu Asp
152                     35                  40                  45
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153
154     Arg Ile Cys Pro Lys Cys Arg Ala Asp Asn Leu His Pro Val Ser
155                     50              55                      60
156
157     Pro Gly Ser Pro Leu Thr Gln Glu Lys Val His Ser Asp Val Ala
158                     65              70                      75
159
160     Glu Ala Glu Ile Met Cys Pro Phe Ala Gly Val Gly Cys Ser Phe
161                     80              85                      90
162
163     Lys Gly Ser Pro Gln Ser Met Gln Glu His Glu Ala Thr Ser Gln
164                     95              100                     105
165
166     Ser Ser His Leu Tyr Leu Leu Leu Ala Val Leu Lys Glu Trp Lys
167                     110             115                     120
168
169     Ser Ser Pro Gly Ser Asn Leu Gly Ser Ala Pro Met Ala Leu Glu
170                     125             130                     135
171
172     Arg Asn Leu Ser Glu Leu Gln Leu Gln Ala Ala Val Glu Ala Thr
173                     140             145                     150
174
175     Gly Asp Leu Glu Val Asp Cys Tyr Arg Ala Pro Cys Cys Glu Ser
176                     155             160                     165
177
178     Gln Glu Glu Leu Ala Leu Gln His Leu Val Lys Glu Lys Leu Leu
179                     170             175                     180
180
181     Ala Gln Leu Glu Glu Lys Leu Arg Val Phe Ala Asn Ile Val Ala
182                     185             190                     195
183
184     Val Leu Asn Lys Glu Val Glu Ala Ser His Leu Ala Leu Ala Ala
185                     200             205                     210
186
187     Ser Ile His Gln Ser Gln Leu Asp Arg Glu His Leu Leu Ser Leu
188                     215             220                     225
189
190     Glu Gln Arg Val Val Glu Leu Gln Gln Thr Leu Ala Gln Lys Asp
191                     230             235                     240
192
193     Gln Val Leu Gly Lys Leu Glu His Ser Leu Arg Leu Met Glu Glu
194                     245             250                     255
195
196     Ala Ser Phe Asp Gly Thr Phe Leu Trp Lys Ile Thr Asn Val Thr
197                     260             265                     270
198
199     Lys Arg Cys His Glu Ser Val Cys Gly Arg Thr Val Ser Leu Phe
200                     275             280                     285
201
202     Ser Pro Ala Phe Tyr Thr Ala Lys Tyr Gly Tyr Lys Leu Cys Leu
203                     290             295                     300
204
205     Arg Leu Tyr Leu Asn Gly Asp Gly Ser Gly Lys Lys Thr His Leu
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INPUT SET: S15900.raw

```
206                    305              310              315
207
208   Ser Leu Phe Ile Val Ile Met Arg Gly Glu Tyr Asp Ala Leu Leu
209                    320              325              330
210
211   Pro Trp Pro Phe Arg Asn Lys Val Thr Phe Met Leu Leu Asp Gln
212                    335              340              345
213
214   Asn Asn Arg Glu His Ala Ile Asp Ala Phe Arg Pro Asp Leu Ser
215                    350              355              360
216
217   Ser Ala Ser Phe Gln Arg Pro Gln Ser Glu Thr Asn Val Ala Ser
218                    365              370              375
219
220   Gly Cys Pro Leu Phe Phe Pro Leu Ser Lys Leu Gln Ser Pro Lys
221                    380              385              390
222
223   His Ala Tyr Val Lys Asp Asp Thr Met Phe Leu Lys Cys Ile Val
224                    395              400              405
225
226   Asp Thr Ser Ala
227              409
228
229   (2) INFORMATION FOR SEQ ID NO:3:
230
231      (i) SEQUENCE CHARACTERISTICS:
232          (A) LENGTH: 2121 base pairs
233          (B) TYPE: Nucleic Acid
234          (C) STRANDEDNESS: Single
235          (D) TOPOLOGY: Linear
236
237      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
238
239
240   GCGCGAAGAC CGTTGGGGCT TTGTGGTGTG TGGGGGTTGT AACTCACATG  50
241
242   GCTGCAGCCA GTGTGACTTC CCCTGGCTCC CTAGAACTGC TACAGCCTGG  100
243
244   CTTCTCCAAG ACCCTCCTGG GGACCAGGTT AGAAGCCAAG TACCTCTGTT  150
245
246   CAGCCTGCAA AAACATCCTG CGGAGGCCTT TCCAGGCCCA GTGTGGGCAC  200
247
248   CGCTACTGCT CCTTCTGCCT GACCAGCATC CTCAGCTCTG GGCCCCAGAA  250
249
250   CTGTGCTGCC TGTGTCTATG AAGGCCTGTA TGAAGAAGGC ATTTCTATTT  300
251
252   TAGAGAGTAG TTCGGCCTTT CCAGATAACG CTGCCCGCAG AGAGGTGGAG  350
253
254   AGCCTGCCAG CTGTCTGTCC CAATGATGGA TGCACTTGGA AGGGGACCTT  400
255
256   GAAAGAATAC GAGAGCTGCC ACGAAGGACT TTGCCCATTC CTGCTGACGG  450
257
258   AGTGTCCTGC ATGTAAAGGC CTGGTCCGCC TCAGCGAGAA GGAGCACCAC  500
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SEQUENCE VERIFICATION REPORT
PATENT APPLICATION   *US/08/779,599*

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